CLAIMS

1. An isolated nucleic acid containing at least twenty-seven nucleotides wherein the nucleotide sequence for said nucleic acid is selected from the group consisting of:

(a) SEQ. ID. NOS.: 1, 5, and 27-49 and nucleotide sequences complementary to SEQ. ID. NOS.: 1, 5 and 27-49;

(b) nucleotide sequences that hybridize under standard stringent hybridization conditions to one or more of the following nucleotide sequences: SEQ. ID. NOS.: 1, 5, and 27-49 and the respective complements of SEQ. ID. NOS.: 1, 5 and 27-49; and

(c) nucleotide sequences that but for the degeneracy of the genetic code would hybridize under standard stringent hybridization conditions to one or more of the following nucleotide sequences: SEQ. ID. NOS.: 1, 5, and 27-49 and the respective complements of SEQ. ID. NOS.: 1, 5 and 27-49.

2. An isolated nucleic acid according to Claim 1 which encodes an MN protein or polypeptide.

3. An isolated nucleic acid according to Claim 1 which contains at least fifty nucleotides.

4. An isolated nucleic acid according to Claim 1 which contains at least 100 nucleotides.

5. An isolated nucleic acid according to Claim 1 which contains at least 150 nucleotides

6. An isolated nucleic acid according to Claim 1 which functions to identify MN nucleic acids.

7. An isolated nucleic acid according to Claim 1 containing at least fifty nucleotides which is selected from the group consisting of:

(a) SEQ. ID. NO.: 1;

(b) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 1 or to its complementary strand; and

(c) nucleotide sequences that differ from SEQ. ID. NO.: 1 and/or from the nucleotide sequences of (b) in codon sequence due to the degeneracy of the genetic code.

8. The isolated nucleic acid according to Claim 7 wherein the selected nucleotide sequence is SEQ. ID. NO.: 1.

9. An isolated nucleic acid according to Claim 1 containing at least fifty nucleotides which is selected from the group consisting of:

(a) SEQ. ID. NOS.: 28, 30-35, 37 and 38;

(b) nucleotide sequences that hybridize under standard stringent hybridization conditions to the sequences of (a) or to their respective complements; and

(c) nucleotide sequences that differ from the sequences of (a) and (b) in codon sequence due to the degeneracy of the genetic code.

10. An isolated nucleic acid according to Claim 1 which is selected from the group consisting of:

(a) SEQ. ID. NOS.: 29 and 36 and their respective complements; and

(b) degenerative variants of the sequences of (a).

11. An isolated nucleic acid according to Claim 1 wherein said nucleotide sequence is selected from the group consisting of:

(a) SEQ. ID. NO.: 5 and its complement;

(b) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 5 or to its complement;

(c) nucleotide sequences that differ from the nucleotide sequences of (a) or (b) in codon sequence due to the degeneracy of the genetic code.

12. An isolated nucleic acid according to Claim 1 wherein said nucleotide sequence is selected from the group consisting of:

(b) SEQ. ID. NO.: 27 and its complement;

(b) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 27 or to its complement; and

(c) nucleotide sequences that differ from the nucleotide sequence of (a) or (b) in codon sequence due to the degeneracy of the genetic code.

13. An isolated nucleic acid containing at least sixteen nucleotides wherein the nucleotide sequence therefor is selected from the group consisting of:

(a) the MN nucleotide sequences contained in plasmids A4a, XE1 and XE3 which were deposited at the American Type Culture Collection (ATCC) in Rockville, Maryland in the United State of America under the respective ATCC Nos. _____, _____, and _____;

(b) nucleotide sequences that hybridize under stringent conditions to the MN nucleotide sequences of (a); and

(c) nucleotide sequences that differ from the nucleotide sequences of (a) or (b) in codon sequence due to the degeneracy of the genetic code.

14. An isolated nucleic acid according to Claim 13 which contains at least twenty-seven nucleotides.

15. An isolated nucleic acid according to Claim 13 which functions as a polymerase chain reaction primer for MN.

16. An isolated nucleic acid according to Claim 15 which is from 16 to 50 nucleotides in length.

17. The isolated nucleic acid according to Claim 1 wherein said nucleic acid or a fragment thereof is a polymerase chain reaction primer useful in amplifying segments of MN genes wherein said primer hybridizes under stringent conditions to nucleic acid sequences encoding MN proteins or polypeptides or to the sequences complementary to those encoding MN proteins or polypeptides.

18. An isolated nucleic acid, containing at least fifty nucleotides, encoding an MN protein or polypeptide that is specifically bound either by monoclonal antibodies designated M75 secreted by the hybridoma VU-M75 deposited at

the American Type Culture Collection (ATCC) in Rockville, Maryland in the United States of America under ATCC No. HB 11128, or by monoclonal antibodies designated MN12 secreted by the hybridoma MN 12.2.2 deposited at the ATCC under ATCC No. 11647, or by both of said monoclonal antibodies.

19. An isolated nucleic acid according to Claim 1 operatively linked to an expression control sequence within a vector.

20. A unicellular host which is either prokaryotic or eukaryotic that is transformed or transfected with the isolated nucleic acid operatively linked to an expression control sequence in a vector according to Claim 19.

21. A unicellular host according to Claim 20 which is an insect cell or an E. coli cell.

22. A method of recombinantly producing an MN protein or MN polypeptide comprising the steps of:

(a) transforming a unicellular host with the isolated nucleic acid operatively linked to an expression control sequence in a vector according to Claim 19;

(b) culturing said unicellular host so that said MN protein or polypeptide is expressed; and

(c) extracting and isolating said MN protein or polypeptide.

23. A method of recombinantly producing an MN protein or polypeptide according to Claim 22 wherein a baculovirus expression system is used.

24. The isolated nucleic acid according to Claim 1 wherein fragments of said nucleic acid are polymerase chain reaction primers for segments of MN genes wherein said primers specifically hybridize under stringent conditions to nucleic acid sequences encoding MN proteins or to sequences complementary to those encoding MN proteins, but do not hybridize under stringent conditions to nucleic acid sequences encoding carbonic anhydrase proteins or to sequences complementary to those encoding carbonic anhydrase proteins.

25. An isolated nucleic acid which functions as a polymerase chain reaction primer for MN according to Claim 24 which are selected from the group consisting of:

(a) SEQ. ID. NOS.: 3, 4, 7, 8, 9, 17 and 18 and their respective complements;

(b) sequences that hybridize to the sequences of (a) under standard stringent hybridization conditions; and

(c) sequences that differ from the sequences of (a) or (b) in codon sequence due to the degeneracy of the genetic code.

26. A nucleic acid probe which is selected from the group consisting of:

(a) SEQ. ID. NO.: 1 or its complement;

(b) SEQ. ID. NO.: 5 or its complement;

(c) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 1 or to its complement;

(d) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 5 or to its complement; and

(e) degenerate variants of SEQ. ID. NO.: 1 and of SEQ. ID. NO.: 5, and of the nucleotide sequences of (c) and (d); and

wherein said nucleic acid probe contains at least twenty-nine nucleotides.

27. The nucleic acid probe according to Claim 26 which is SEQ. ID. NO.: 1 or SEQ. ID. NO.: 5.

28. A test kit comprising the nucleic acid probe according to Claim 26 and a means to enable the

visualization of said nucleic acid probe once hybridized to its target nucleic acid sequence.

29. An isolated nucleic acid, containing at least twenty-nine nucleotides, encoding an MN protein or polypeptide to which monoclonal antibodies designated M75 or MN12 produced respectively by the hybridomas VU-M75 and MN 12.2.2 deposited at the American Type Culture Collection (ATCC) in Rockville, Maryland in the United States of America under respective ATCC No. HB 11128 and 11647, specifically bind, wherein the nucleotide sequence for said nucleic acid is selected from the group consisting of:

(a) SEQ. ID. NO.: 1;

(b) SEQ. ID. NO.: 5;

(c) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 1 or to its complement;

(d) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 5 or to its complement; and

(e) degenerate variants of SEQ. ID. NO.: 1 and of SEQ. ID. NO.: 5, and of the nucleotide sequences of (c) and (d).

30. A recombinant nucleic acid encoding a fusion protein consisting essentially of an MN protein or

polypeptide and a non-MN protein or polypeptide wherein the nucleotide sequence for the portion of the nucleic acid encoding the MN protein or polypeptide is selected from the group consisting of:

(a) SEQ. ID. NO.: 1;

(b) SEQ. ID. NO.: 5;

(c) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 1 or to its complement;

(d) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 5 or to its complement; and

(e) degenerate variants of SEQ. ID. NO.: 1, of SEQ. ID. NO.: 5, and of the nucleotide sequences of (c) and (d); and

wherein the nucleic acid encoding said MN protein or polypeptide contains at least twenty-nine nucleotides.

31. The recombinant nucleic acid encoding a fusion protein according to Claim 30 wherein the non-MN protein or polypeptide is not immunogenic.

32. The recombinant nucleic acid according to Claim 30 wherein the non-MN protein or polypeptide is immunogenic.

33. The recombinant nucleic acid according to Claim 30 which is contained in a vector.

34. The recombinant nucleic acid according to Claim 30 wherein said non-MN protein is the alpha-peptide region of beta-galactosidase, the carboxyl terminus of glutathione S-transferase, a Protein A fragment, or a Fc fragment.

35. A method of detecting mutations in an isolated MN gene and/or fragment(s) thereof comprising the steps of:

amplifying one or more fragment(s) of said gene by the polymerase chain reaction (PCR); and

determining whether said one or more fragments contain any mutations.

36. A method according to Claim 35 wherein said fragments of MN genes are isolated from one or more people without neoplastic disease and from one or more people with neoplastic disease, and the amplified fragments are compared for differences in size.

37. A method according to Claim 35 comprising the use of a PCR-single-strand conformation polymorphism assay or a denaturing gradient gel electrophoretic assay to

determine whether said one or more fragments contain any mutations.